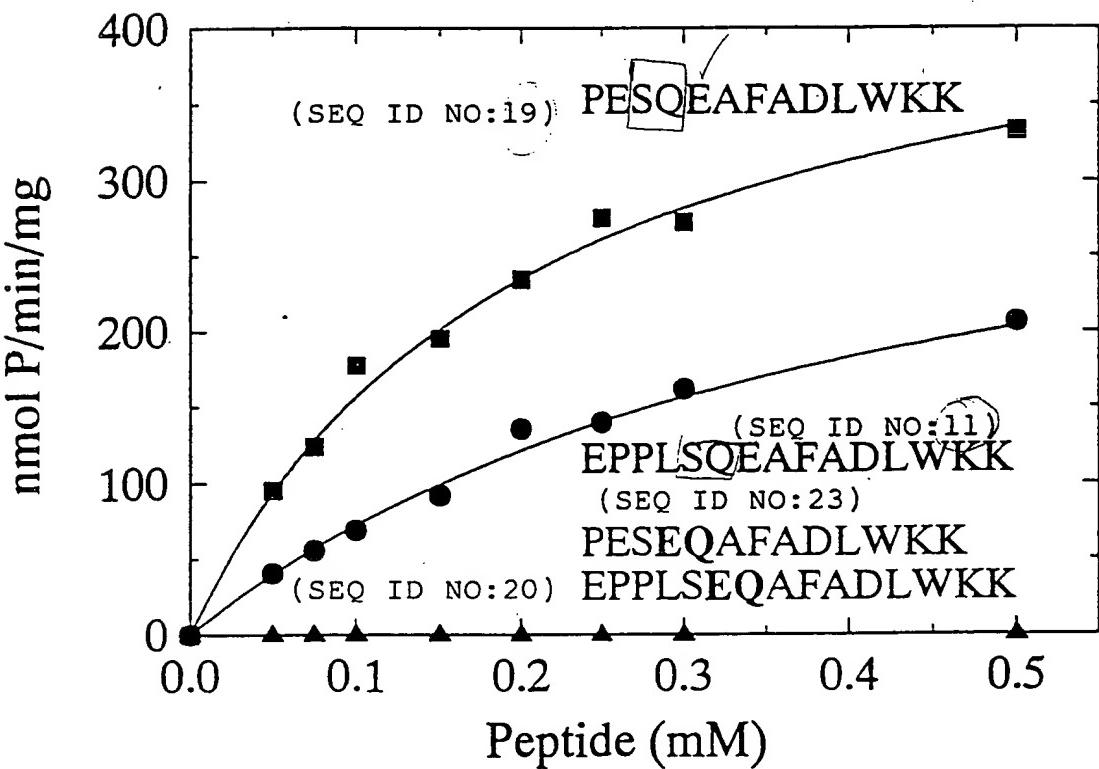


FIGURE 1

Phosphorylation of Synthetic Peptides by Human DNA-PK



0046207 - 2005062960

FIGURE 2

Phosphorylation of Synthetic Peptides by Purified Human DNA-PK

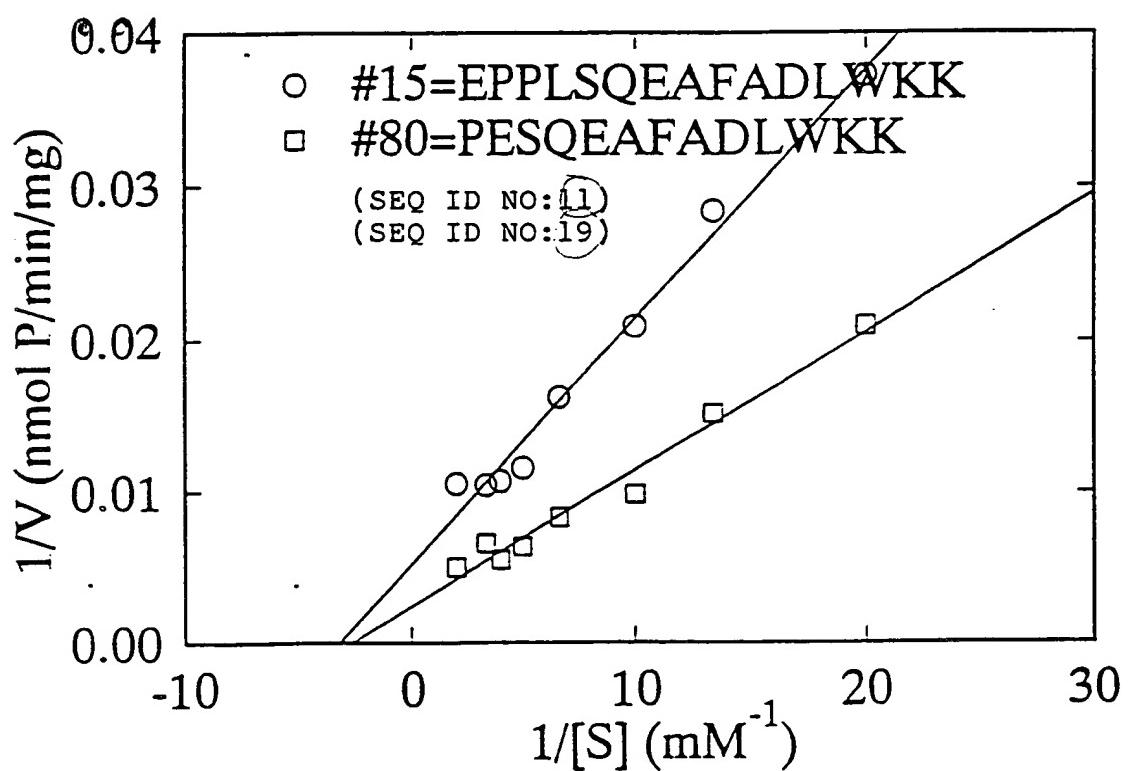


FIGURE 3

Phosphorylation of Synthetic Peptides by Human DNA-PK

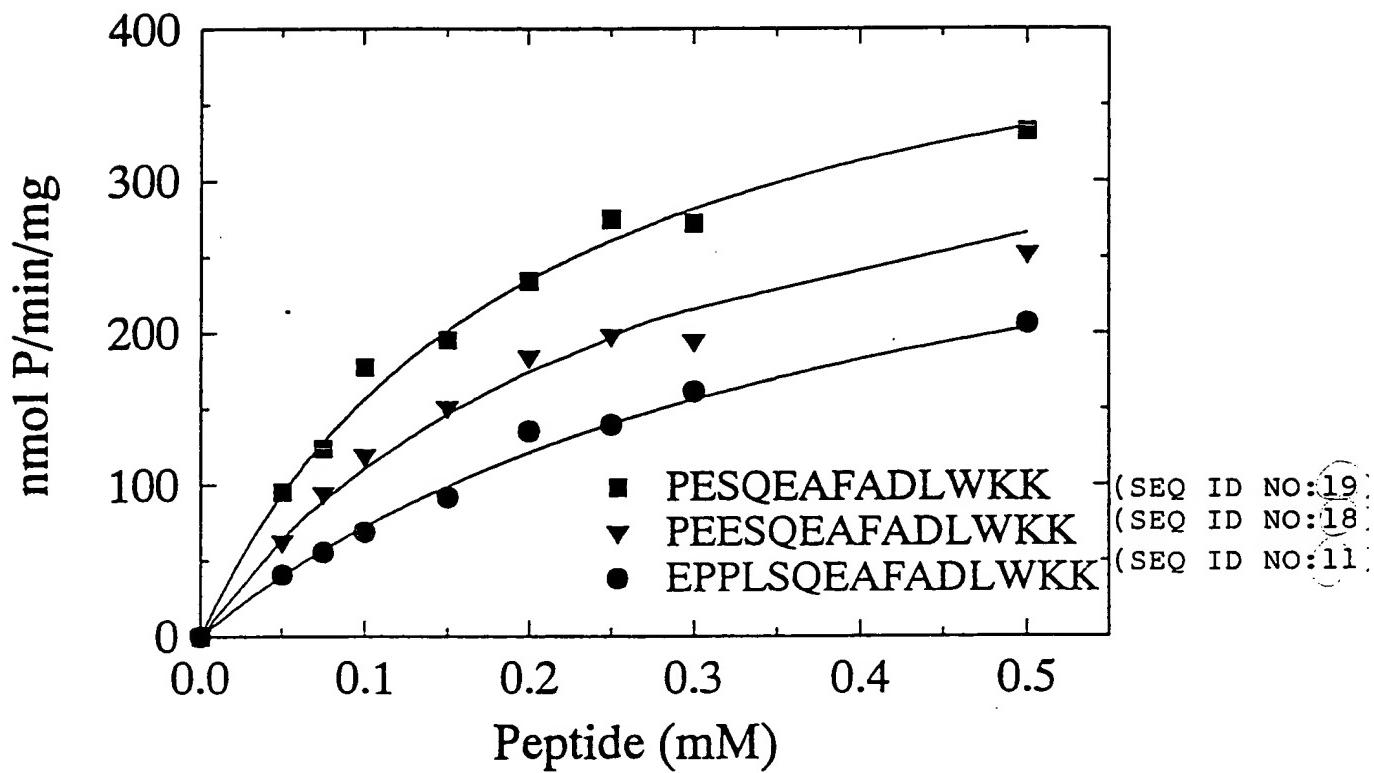


FIGURE 4

Artificial DNA-PK Substrates

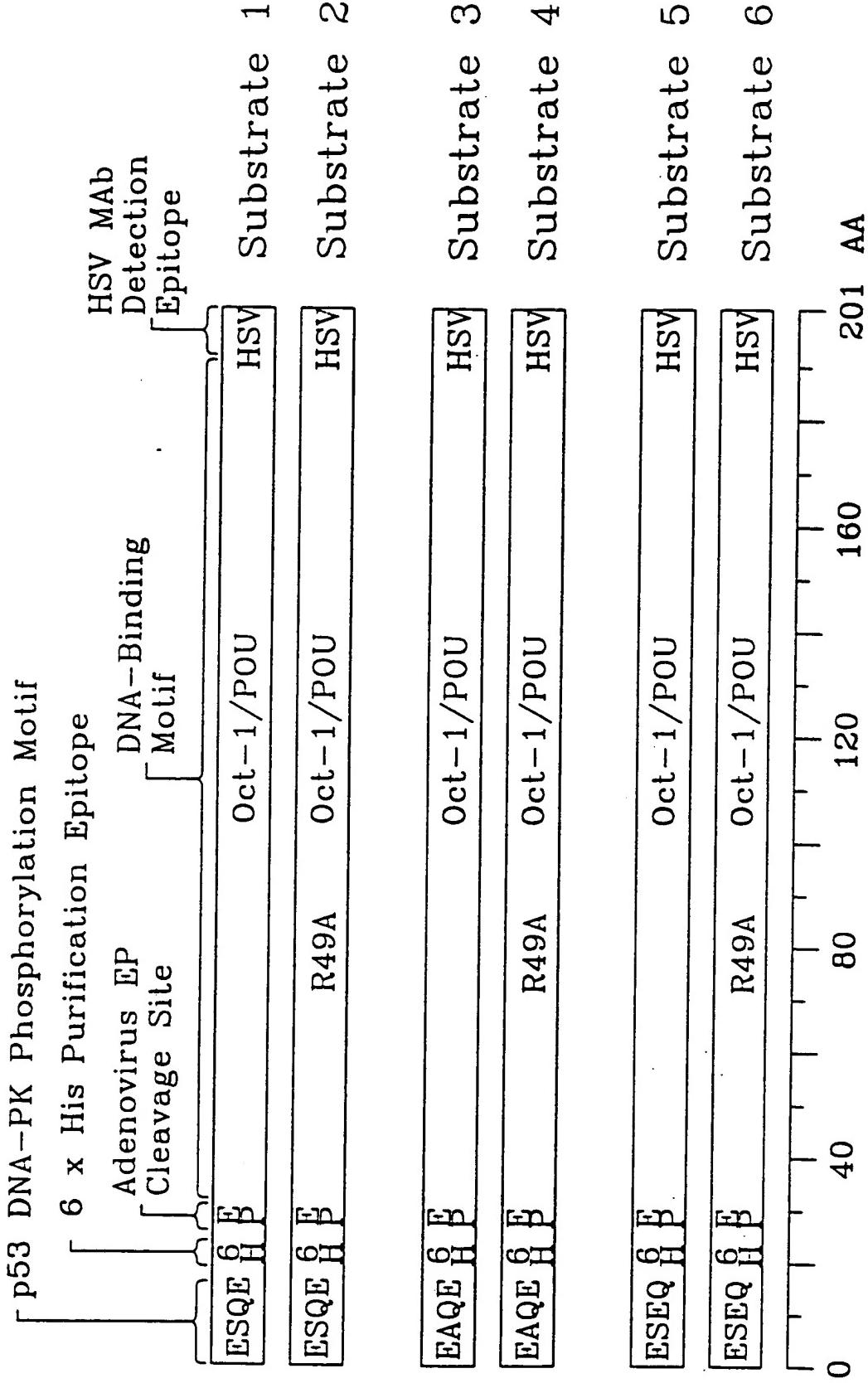


FIGURE 5A

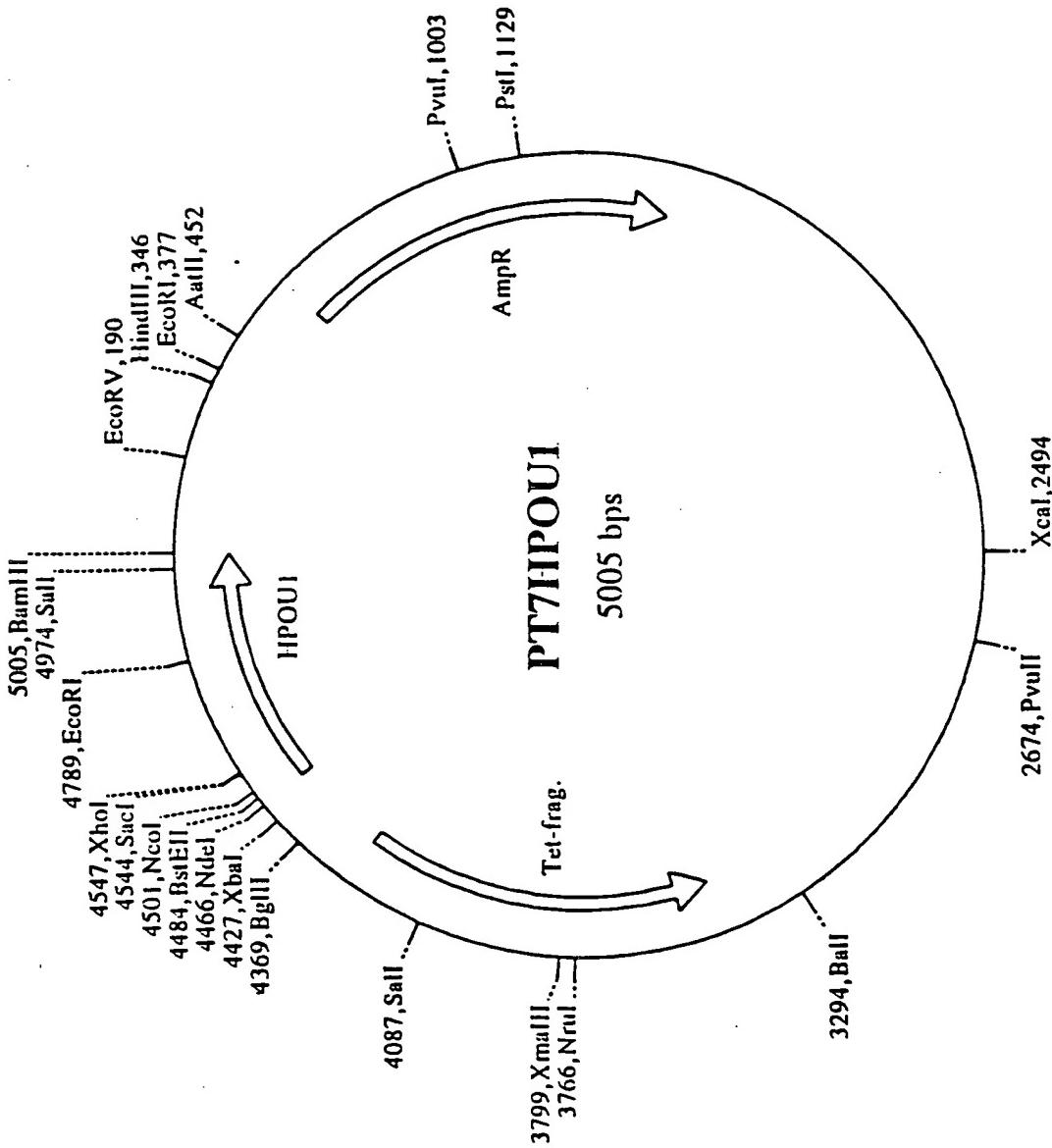


FIGURE 5B

Expressed Prot in Product of pT7HPOU1

pT7HPOU1: Expression Vector for Human Oct-1 POU Domain with His6 leader
T7HPOU1 5005 bases, circular

Lab Strain: #236 = pT7HPOU1/DH5[alpha]
Lab Strain: #237 = pT7HPOU1/BL21(DE3)

Plasmid Construction:

Vector: pT7HIS2 (pET-3 with His6 leader and T7 gene 2.5)
Cut with Nco I and BamH I

Insert: POU domain from pET11c-OCT1POU (CWA Strain #234) from Winship Herr, Cold Spring Harbor Laboratory. POU domain DNA was made by PCR using primers #761 and #430 (pBR322 EcoR I site). PCR fragment was cut with NcoI and BamHI, purified, and inserted in similarly cut pT7HIS2 vector (also called pT7AdEP-DBP).

PREDICTED PROTEIN SEQUENCE OF EXPRESSION PRODUCT Segment: 4469-5005

(SEQ ID NO:59)

Composition

8 Ala	7 Gln	18 Leu	18 Ser
12 Arg	17 Glu	15 Lys	9 Thr
11 Asn	11 Gly	8 Met	2 Trp
6 Asp	6 His	8 Phe	1 Tyr
2 Cys	9 Ile	6 Pro	4 Val

Mol. wt. unmod. chain = 20,352 Number of residues = 178

Met Ala Ser Met Thr Gly His His His His His Gly Met Ser Gly
1 5 10 15

Gly Met Glu Glu Pro Ser Asp Leu Glu Glu Leu Glu Gln Phe Ala Lys
20 25 30

Thr Phe Lys Gln Arg Arg Ile Lys Leu Gly Phe Thr Gln Gly Asp Val
35 40 45

Gly Leu Ala Met Gly Lys Leu Tyr Gly Asn Asp Phe Ser Gln Thr Thr
50 55 60

FIGURE 5B (Continued)

(SEQ ID NO:59)

Ile Ser Arg Phe Glu Ala Leu Asn Leu Ser Phe Lys Asn Met Cys Lys
65 70 75 80

Leu Lys Phe Leu Leu Glu Lys Trp Leu Asn Asp Ala Glu Asn Leu Ser
85 90 95

Ser Asp Ser Ser Leu Ser Ser Pro Ser Ala Leu Asn Ser Pro Gly Ile
100 105 110

Glu Gly Leu Ser Arg Arg Arg Lys Lys Arg Thr Ser Ile Glu Thr Asn
115 120 125

Ile Arg Val Leu Glu Lys Ser Phe Leu Glu Asn Gln Lys Pro Thr Ser
130 135 140

Glu Glu Ile Thr Met Ile Ala Asp Gln Leu Asn Met Glu Lys Glu Val
145 150 155 160

Ile Arg Val Trp Phe Cys Asn Arg Arg Gln Lys Glu Lys Arg Ile Asn
165 170 175

Pro

Reference: Anderson, C. W., and S. P. Lees-Miller. 1992. The nuclear serine/threonine protein kinase DNA-PK. Crit. Rev. Eukaryotic Gene Express. 2, 283-314.

Figure 5C

NUCLEOTIDE SEQUENCE OF pT7HPOU1

(SEQ ID NO:60)

GATCCACAGG ACGGGTGTGG TCGCCATGAT CGCGTAGTCG ATAGTGGCTC CAAGTAGCGA 60
AGCGAGCAGG ACTGGGCGGC GGCCAAAGCG GTCGGACAGT GCTCCGAGAA CGGGTGCGCA 120
TAGAAATTGC ATCAACGCAT ATAGCGCTAG CAGCACGCCA TAGTGACTGG CGATGCTGTC 180
GGAATGGACG ATATCCCGCA AGAGGCCCGG CAGTACCGGC ATAACCAAGC CTATGCCTAC 240
AGCATCCAGG GTGACGGTGC CGAGGATGAC GATGAGCGCA TTGTTAGATT TCATACACGG 300
TGCCTGACTG CGTTAGCAAT TTAACTGTGA TAAACTACCG CATTAAAGCT TATCGATGAT 360
AAGCTGTCAA ACATGAGAAT TCTTGAAGAC GAAAGGGCCT CGTGATACGC CTATTTTAT 420
AGGTTAACATGT CATGATAATA ATGGTTTCTT AGACGTCAGG TGGCACTTTT CGGGGAAATG 480
TGCGCGAAC CCCTATTTGT TTATTTTCT AAATACATTC AAATATGTAT CCGCTCATGA 540
GACAATAACC CTGATAAAATG CTTCAATAAT ATTGAAAAAG GAAGAGTATG AGTATTCAAC 600
ATTTCCGTGT CGCCCTTATT CCCTTTTTG CGGCATTTG CCTTCCTGTT TTTGCTCACC 660
CAGAAACGCT GGTGAAAGTA AAAGATGCTG AAGATCAGTT GGGTGCACGA GTGGGTTACA 720
TCGAACTGGA TCTAACAGC GGTAAGATCC TTGAGAGTTT TCGCCCCGAA GAACGTTTC 780
CAATGATGAG CACTTTAAA GTTCTGCTAT GTGGCGCGGT ATTATCCCGT GTGACGCCG 840
GGCAAGAGCA ACTCGGTGCG CGCATACACT ATTCTCAGAA TGACTTGGTT GAGTACTCAC 900
CAGTCACAGA AAAGCATCTT ACGGATGGCA TGACAGTAAG AGAATTATGC AGTGCTGCCA 960
TAACCATGAG TGATAACACT GC GGCCA ACT TACTCTGAC AACGATCGGA GGACCGAAGG 1020
AGCTAACCGC TTTTTGCAC AACATGGGGG ATCATGTAAC TCGCCTGAT CGTTGGGAAC 1080
CGGAGCTGAA TGAAGCCATA CCAAACGACG AGCGTGACAC CACGATGCCCT GCAGCAATGG 1140
CAACAAACGTT GCGCAAACTA TTAACTGGCG AACTACTTAC TCTAGCTTCC CGGCAACAAT 1200
TAATAGACTG GATGGAGGCG GATAAAGTTG CAGGACCACT TCTGCGCTCG GCCCTTCCGG 1260
CTGGCTGGTT TATTGCTGAT AAATCTGGAG CCGGTGAGCG TGGGTCTCGC GGTATCATTG 1320
CAGCACTGGG GCCAGATGGT AAGCCCTCCC GTATCGTAGT TATCTACACG ACGGGGAGTC 1380

Figure 5C (Continued)

(SEQ ID NO:60)

AGGCAACTAT GGATGAACGA AATAGACAGA TCGCTGAGAT AGGTGCCTCA CTGATTAAGC 1440
ATTGGTAACT GTCAGACCAA GTTTACTCAT ATATACTTTA GATTGATTTA AAACTTCATT 1500
TTTAATTTAA AAGGATCTAG GTGAAGATCC TTTTGATAA TCTCATGACC AAAATCCCTT 1560
AACGTGAGTT TTCGTTCCAC TGAGCGTCAG ACCCCGTAGA AAAGATCAAA GGATCTTCTT 1620
GAGATCCTTT TTTTCTGCGC GTAATCTGCT GCTTGCAAAC AAAAAAAACCA CCGCTACCAG 1680
CGGTGGTTTG TTTGCCGGAT CAAGAGCTAC CAACTCTTT TCCGAAGGTA ACTGGCTTCA 1740
GCAGAGCGCA GATACCAAAT ACTGTCCTTC TAGTGTAGCC GTAGTTAGGC CACCACTTCA 1800
AGAAACTCTGT AGCACCGCCT ACATACCTCG CTCTGCTAAT CCTGTTACCA GTGGCTGCTG 1860
CCAGTGGCGA TAAGTCGTGT CTTACCGGGT TGGACTCAAG ACGATAGTTA CCGGATAAGG 1920
CGCAGCGGTC GGGCTGAACG GGGGGTTCGT GCACACAGCC CAGCTTGGAG CGAACGACCT 1980
ACACCGAAGT GAGATACCTA CAGCGTGAGC ATTGAGAAAG CGCCACGCTT CCCGAAGGGA 2040
GAAAGGCGGA CAGGTATCCG GTAAGCGGCA GGGTCGGAAC AGGAGAGCGC ACGAGGGAGC 2100
TTCCAGGGGG AAACGCCCTGG TATCTTTATA GTCCTGTCGG GTTTCGCCAC CTCTGACTTG 2160
AGCGTCGATT TTTGTGATGC TCGTCAGGGG GGCGGAGCCT ATGGAAAAAC GCCAGCAACG 2220
CGGCCCTTTT ACGGTTCCCTG GCCTTTGCT GGCCTTTGC TCACATGTTTC TTTCCTGCGT 2280
TATCCCCTGA TTCTGTGGAT AACCGTATTA CCGCCTTTGA GTGAGCTGAT ACCGCTCGCC 2340
GCAGCCGAAC GACCGAGCGC AGCGAGTCAG TGAGCGAGGA AGCGGAAGAG CGCCTGATGC 2400
GGTATTTCT CCTTACGCAT CTGTGCGGT A TTTCACACCG CATATATGGT GCACTCTCAG 2460
TACAATCTGC TCTGATGCCG CATAGTTAAG CCAGTATACA CTCCGCTATC GCTACGTGAC 2520
TGGGTATGG CTGCGCCCCG ACACCCGCCA ACACCCGCTG ACGCGCCCTG ACAGGGCTTGT 2580
CTGCTCCCGG CATCCGCTTA CAGACAAGCT GTGACCGTCT CCGGGAGCTG CATGTGTCAG 2640
AGGTTTTCAC CGTCATCACC GAAACCGCG AGGCAGCTGC GGTAAAGCTC ATCAGCGTGG 2700
TCGTGAAGCG ATTCAACAGAT GTCTGCCTGT TCATCCGCGT CCAGCTCGTT GAGTTCTCC 2760

Figure 5C (Continued)

(SEQ ID NO:60)

AGAAGCGTTA ATGTCTGGCT TCTGATAAAAG CGGGCCATGT TAAGGGCGGT TTTTCCTGT 2820
TTGGTCACTG ATGCCCTCCGT GTAAGGGGGA TTTCTGTTCA TGGGGGTAAT GATACCGATG 2880
AACCGAGAGA GGATGCTCAC GATACGGGTT ACTGATGATG AACATGCCCG GTTACTGGAA 2940
CGTTGTGAGG GTAAACAACT GGCGGTATGG ATGCGGCGGG ACCAGAGAAA AATCACTCAG 3000
GGTCAATGCC AGCGCTTCGT TAATACAGAT GTAGGTGTT CACAGGGTAG CCAGCAGCAT 3060
CCTGCGATGC AGATCCGGAA CATAATGGTG CAGGGCGCTG ACTTCCGCGT TTCCAGACTT 3120
TACGAAACAC GGAAACCGAA GACCATTCA GTTGTGCTC AGGTCGCAGA CGTTTGAG 3180
CAGCAGTCGC TTCACGTTCG CTCGCGTATC GGTGATTCA TCTGCTAAC AGTAAGGCAA 3240
CCCCGCCAGC CTAGCCGGGT CCTCAACGAC AGGAGCACGA TCATGCGCAC CCGTGGCCAG 3300
GACCCAACGC TGCCCGAGAT GCGCCGCGTG CGGCTGCTGG AGATGGCGGA CGCGATGGAT 3360
ATGTTCTGCC AAGGGTTGGT TTGCGCATTAC ACAGTTCTCC GCAAGAATTG ATTGGCTCCA 3420
ATTCTTGGAG TGGTGAATCC GTTAGCGAGG TGCCGCCGGC TTCCATTCAAG GTCGAGGTGG 3480
CCCGGCTCCA TGCACCGCGA CGCAACGCGG GGAGGCAGAC AAGGTATAGG GCAGCGCCTA 3540
CAATCCATGC CAACCCGTTTC CATGTGCTCG CCGAGGCGGC ATAAATCGCC GTGACGATCA 3600
GCGGTCCAGT GATCGAAGTT AGGCTGGTAA GAGCCGCGAG CGATCCTTGA AGCTGTCCCT 3660
GATGGTCGTC ATCTACCTGC CTGGACAGCA TGGCCTGCAA CGCGGGCATC CCGATGCCGC 3720
CGGAAGCGAG AAGAATCATA ATGGGGAAGG CCATCCAGCC TCGCGTCGCG AACGCCAGCA 3780
AGACGTAGCC CAGCGCGTCG GCCGCCATGC CGCGATAAT GGCTGCTTC TCGCCGAAAC 3840
GTTTGGTGGC GGGACCAGTG ACGAAGGCTT GAGCGAGGGC GTGCAAGATT CCGAATACCG 3900
CAAGCGACAG GCCGATCATC GTCGCGCTCC AGCGAAAGCG GTCCCTGCCG AAAATGACCC 3960
AGAGCGCTGC CGGCACCTGT CCTACGAGTT GCATGATAAA GAAGACAGTC ATAAGTGCAGG 4020
CGACGATAGT CATGCCCGC GCCCACCGA AGGAGCTGAC TGGGTTGAAG GCTCTCAAGG 4080
GCATCGGTGCG ACGCTCTCCC TTATGCGACT CCTGCATTAG GAAGCAGCCC AGTAGTAGGT 4140

Figure 5C (Continued)

(SEQ ID NO:60)

TGAGGCCGTT GAGCACCGCC GCCGCAAGGA ATGGTGCATG CAAGGAGATG GCGCCCAACA 4200
GTCCCCCGGC CACGGGGCCT GCCACCATAAC CCACGCCGAA ACAAGCGCTC ATGAGCCCGA 4260
AGTGGCGAGC CCGATCTTCC CCATCGGTGA TGTCGGCGAT ATAGGCGCCA GCAACCGCAC 4320
CTGTGGCGCC GGTGATGCCG GCCACGATGC GTCCGGCGTA GAGGATCGAG ATCTCGATCC 4380
CGCGAAATTAA ATACGACTCA CTATAGGGAG ACCACAAACGG TTTCCCTCTA GAAATAATTT 4440
TGTTTAACCTT TAAGAAGGGAG ATATACAT ATG GCT TCT ATG ACT GGT CAC CAC 4492
CAC CAT CAC CAT GGT ATG AGC GGC GGC ATG GAG GAG CCC AGT GAC CTT 4540
GAG GAG CTC GAG CAG TTT GCC AAG ACC TTC AAA CAA AGA CGA ATC AAA 4588
CTT GGA TTC ACT CAG GGT GAT GTT GGG CTC GCT ATG GGG AAA CTA TAT 4636
GGA AAT GAC TTC AGC CAA ACT ACC ATC TCT CGA TTT GAA GCC TTG AAC 4684
CTC AGC TTT AAG AAC ATG TGC AAG TTG AAG CCA CTT TTA GAG AAG TGG 4732
CTA AAT GAT GCA GAG AAC CTC TCA TCT GAT TCG TCC CTC TCC AGC CCA 4780
AGT GCC CTG AAT TCT CCA GGA ATT GAG GGC TTG AGC AGG CGC AGG AAG 4828
AAA CGC ACC AGC ATA GAG ACC AAC ATC CGT GTG GCC TTA GAG AAG AGT 4876
TTC TTG GAG AAT CAA AAG CCT ACC TCG GAA GAG ATC ACT ATG ATT GCT 4924
GAT CAG CTC AAT ATG GAA AAA GAG GTG ATT CGT GTT TGG TTC TGT AAC 4972
CGT CGA CAG AAA GAA AAA AGA ATC AAC CCA TAG 5005

FIGURE 6

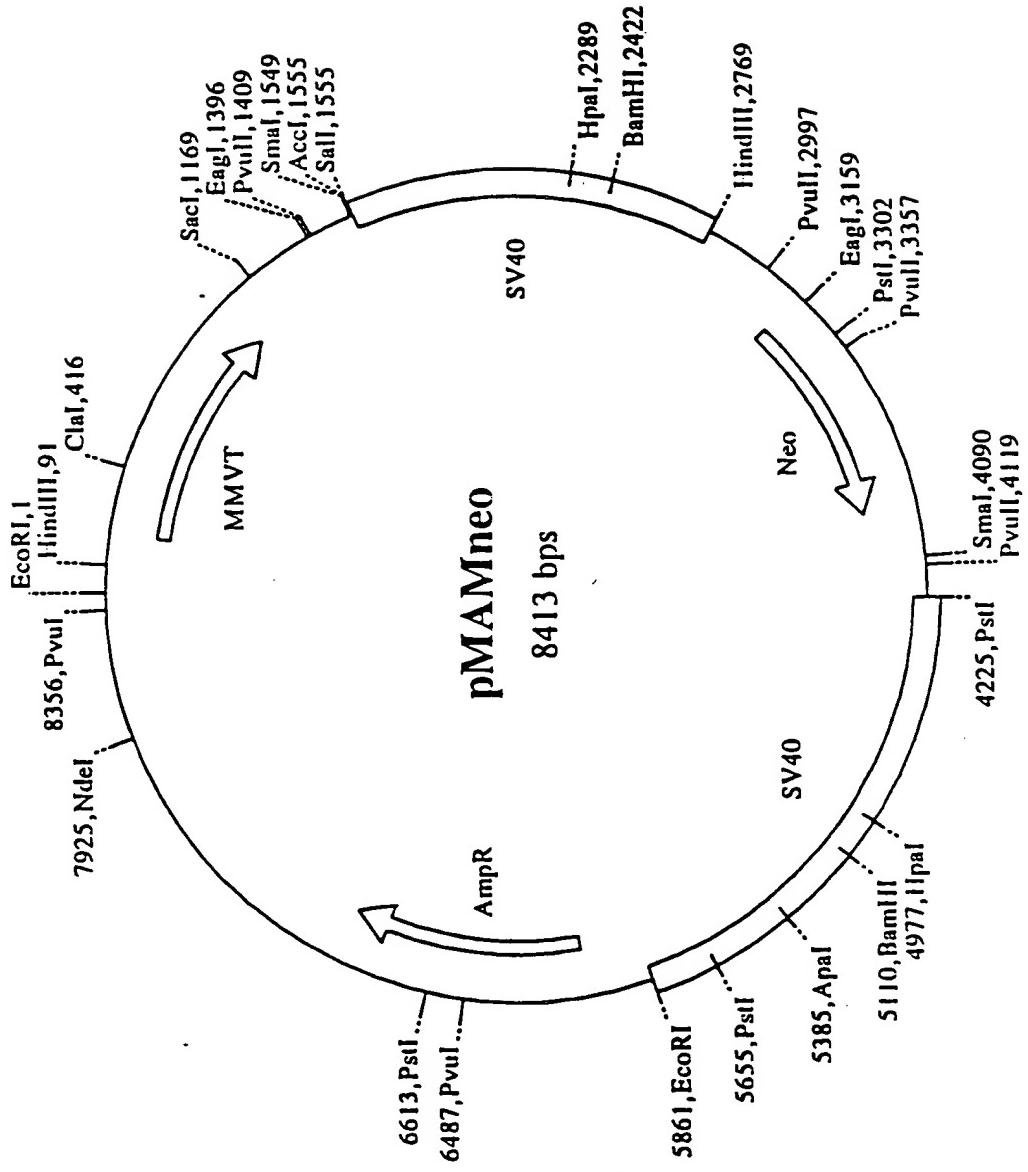


FIGURE 6A

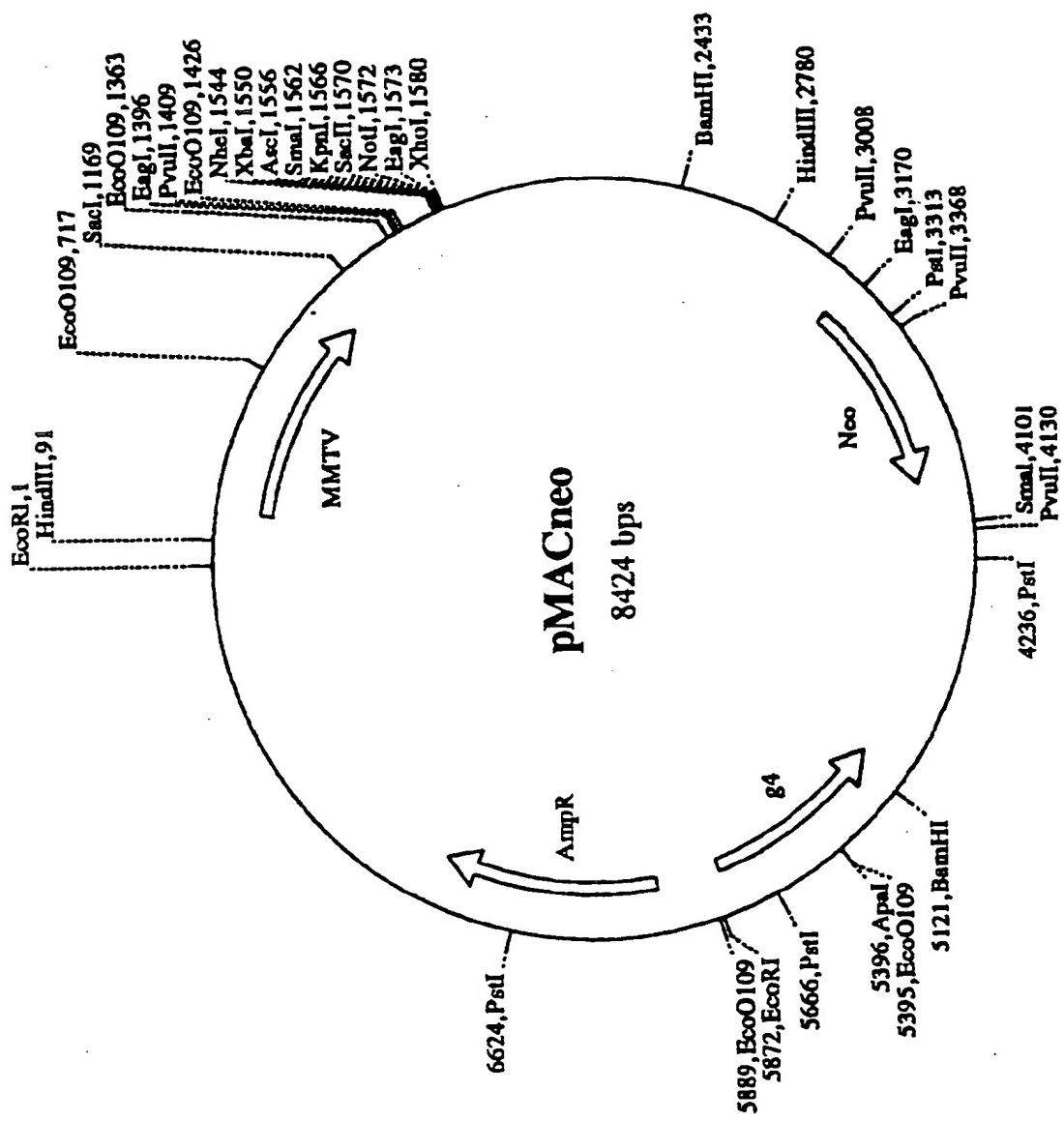


FIGURE 7

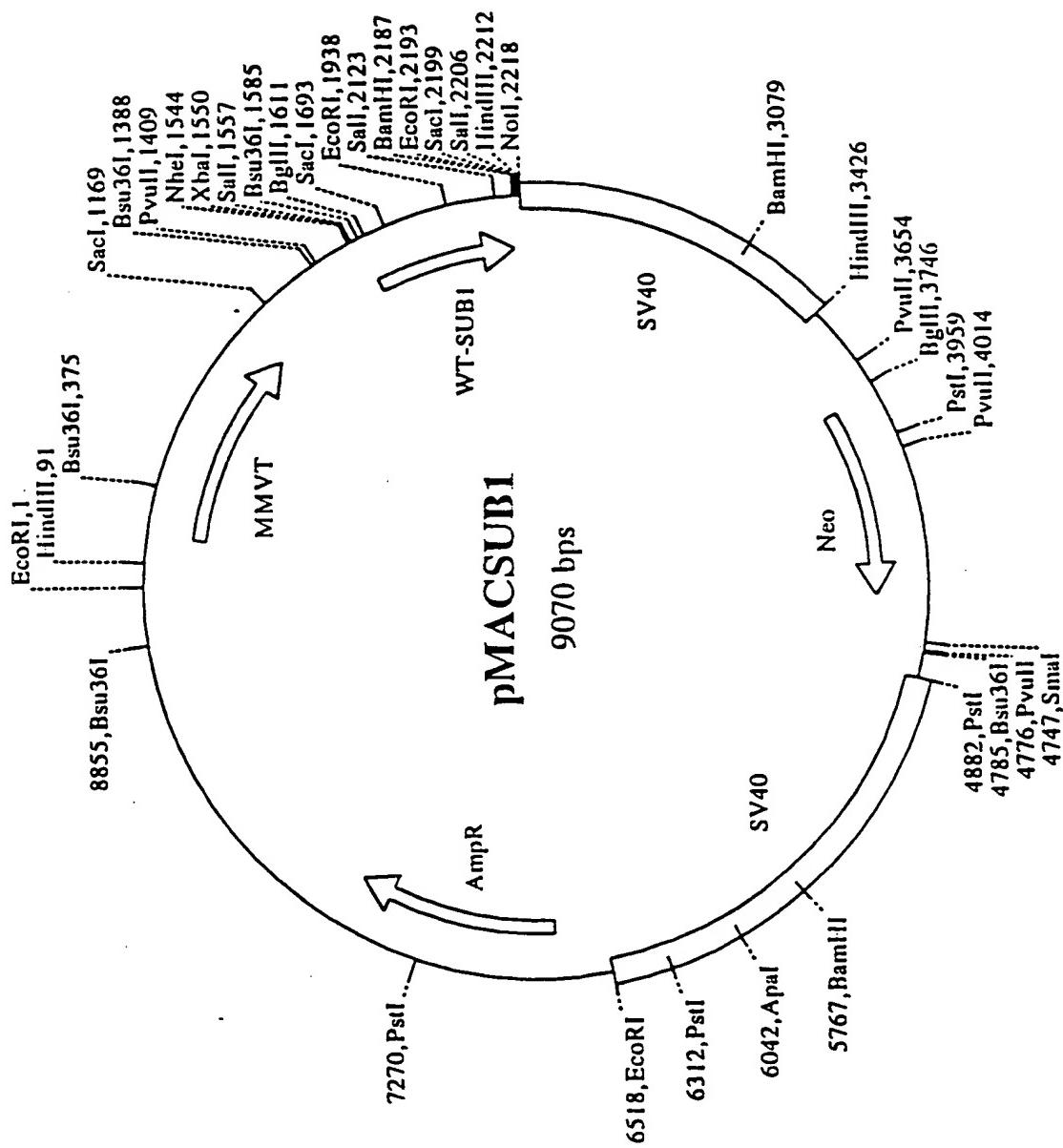


FIGURE 8A

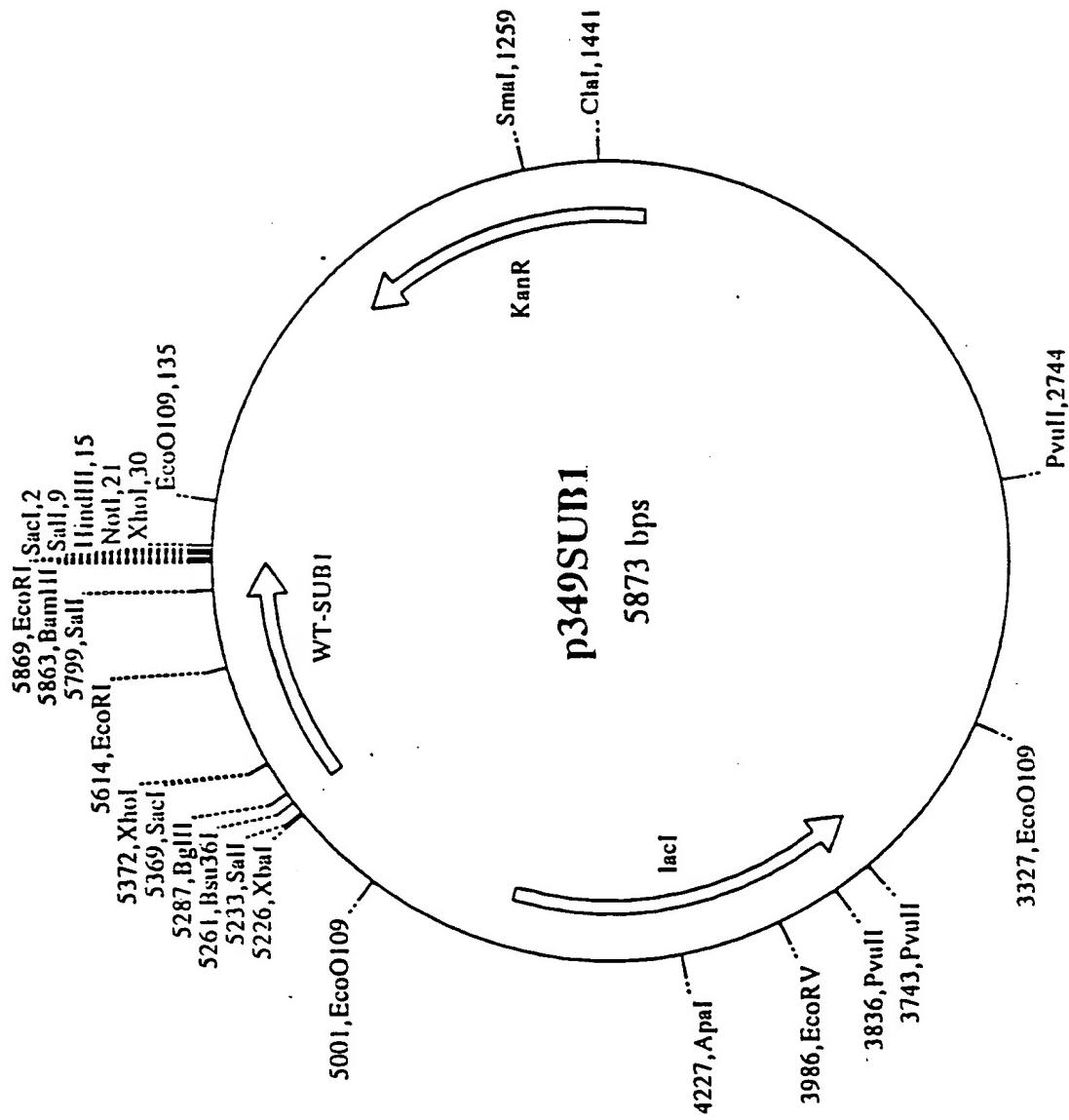


FIGURE 8B

Wild-Type Artificial DNA-PK Substrat 1

Lab Stain: #349 = p349SUB1 in DH5[alpha]
Lab Strain #351 = p349SUB1 in BL21(DE3)

Plasmid Construction:

VECTOR: p410 = derivative pET-28a (Novagen) without BglII site
INSERT: Substrate encoding XbaI-BamHI fragment was excised from p345 with XbaI and BamHI and cloned into XbaI and BamHI cleaved p410.

ANTIBIOTIC SELECTION: 50 ug/ml Kanamycin

PREDICTED SEQUENCE POUSUB1 ARTIFICIAL DNA-PK SUBSTRATE

Segment: 5258-5860

(SEQ ID NO: 61)

Composition

8 Ala	9 Gln	22 Leu	18 Ser
12 Arg	24 Glu	16 Lys	9 Thr
11 Asn	11 Gly	7 Met	3 Trp
9 Asp	6 His	9 Phe	1 Tyr
2 Cys	9 Ile	11 Pro	4 Val

Mol. wt. unmod. chain = 23,126 Number of residues = 201

Met Pro Glu Glu Ser Gln Glu Thr Phe Glu Asp Leu Trp Lys Leu Leu
1 5 10 15

Pro Gly His His His His His Gly Met Ser Gly Gly Met Glu Glu
20 25 30

Pro Ser Asp Leu Glu Glu Leu Glu Gln Phe Ala Lys Thr Phe Lys Gln
35 40 45

Arg Arg Ile Lys Leu Gly Phe Thr Gln Gly Asp Val Gly Leu Ala Met
50 55 60

Gly Lys Leu Tyr Gly Asn Asp Phe Ser Gln Thr Thr Ile Ser Arg Phe
65 70 75 80

Glu Ala Leu Asn Leu Ser Phe Lys Asn Met Cys Lys Leu Lys Pro Leu
85 90 95

Leu Glu Lys Trp Leu Asn Asp Ala Glu Asn Leu Ser Ser Asp Ser Ser
100 105 110

FIGURE 8B (Continued)

(SEQ ID NO:61)

Leu Ser Ser Pro Ser Ala Leu Asn Ser Pro Gly Ile Glu Gly Leu Ser
115 120 125

Arg Arg Arg Lys Lys Arg Thr Ser Ile Glu Thr Asn Ile Arg Val Ala
130 135 140

Leu Glu Lys Ser Phe Leu Glu Asn Gln Lys Pro Thr Ser Glu Glu Ile
145 150 155 160

Thr Met Ile Ala Asp Gln Leu Asn Met Glu Lys Glu Val Ile Arg Val
165 170 175

Trp Phe Cys Asn Arg Arg Gln Lys Glu Lys Arg Ile Asn Pro Gln Pro
180 185 190

Glu Leu Ala Pro Glu Asp Pro Glu Asp
195 200

NOTES:

- Ser 5-Gln 6 = Artificial DNA-PK Site
- Glu 10 = Introduced to make BglII site, =Ser in p53,
=Ala in peptide
- His 19-His 24 = His tag for Zn/Ni-affinity chromatography
- Met 26-Gly 29 = Adenovirus Proteinase Cleavage Motif
- Glu 31-Pro 190 = POU specific domain of Human Oct-1
- Gln 191-Asp 201 = Novagen HSV Epitope Tag

Figure 8C

NUCLEOTIDE SEQUENCE OF p349SUB1

(SEQ ID NO:62)

CGAGCTCCGT CGACAAGCTT GCGGCCGCAC TCGAGCACCA CCACCACCA CACTGAGATC 60
CGGCTGCTAA CAAAGCCCGA AAGGAAGCTG AGTTGGCTGC TGCCACCGCT GAGCAATAAC 120
TAGCATAACC CCTTGGGGCC TCTAACCGGG TCTTGAGGGG TTTTTGCTG AAAGGAGGAA 180
CTATATCCGG ATTGGCGAAT GGGACGCGCC CTGTAGCGGC GCATTAAGCG CGGC GG GT 240
GGTGGTTACG CGCAGCGTGA CCGCTACACT TGCCAGCGCC CTAGCGCCCG CTCCTT CCGC 300
TTTCTTCCCT TCCTTTCTCG CCACGTT CGC CGGCTT CCCC CGTCAAGCTC TAAATCGGGG 360
GCTCCCTTA GGGTCCGAT TTAGTGCTTT ACGGCACCTC GACCCAAAA AACTTGATTA 420
GGGTGATGGT TCACGTAGTG GGCCATCGCC CTGATAGACG GTTTTGCGCC CTTTGACGTT 480
GGAGTCCACG TTCTTAATA GTGGACTCTT GTTCCAAACT GGAACAACAC TCAACCCTAT 540
CTCGGTCTAT TCTTTGATT TATAAGGGAT TTTGCCGATT TCGGCCTATT GGTTAAAAAA 600
TGAGCTGATT TAACAAAAAT TTAACCGCAA TTTAACAAA ATATTAACGT TTACAATTTC 660
AGGTGGCACT TTTGGGGAA ATGTGCGCGG AACCCCTATT TGTTTATTT TCTAAATACA 720
TTCAAATATG TATCCGCTCA TGAATTAATT CTTAGAAAAA CTCATCGAGC ATCAAATGAA 780
ACTGCAATT ATT CATATCA GGATTATCAA TACCATATT TTGAAAAGC CGTTTCTGTA 840
ATGAAGGAGA AAACTCACCG AGGCAGTTCC ATAGGATGGC AAGATCCTGG TATCGGTCTG 900
CGATTCCGAC TCGTCCAACA TCAATACAAC CTATTAATT CCCCTCGTCA AAAATAAGGT 960
TATCAAGTGA GAAATCACCA TGAGTGACGA CTGAATCCGG TGAGAATGGC AAAAGTTTAT 1020
GCATTTCTTT CCAGACTTGT TCAACAGGCC AGCCATTACG CTCGTCACTCA AAATCACTCG 1080
CATCAACCAA ACCGTTATTC ATT CGTGATT GCGCCTGAGC GAGACGAAAT ACGCGATCGC 1140
TGTAAAAGG ACAATTACAA ACAGGAATCG AATGCAACCG GCGCAGGAAC ACTGCCAGCG 1200
CATCAACAAT ATTTCACCT GAATCAGGAT ATTCTTCTAA TACCTGGAAT GCTGTTTCC 1260
CGGGGATCGC AGTGGTGAGT AACCATGCAT CATCAGGAGT ACGGATAAAA TGCTTGATGG 1320
TCGGAAGAGG CATAAATTCC GTCAGCCAGT TTAGTCTGAC CATCTCATCT GTAACATCAT 1380

Figure 8C (Continued)

(SEQ ID NO:62)

TGGCAACGCT ACCTTTGCCA TGTTTCAGAA ACAACTCTGG CGCATCGGGC TTCCCATACA 1440
ATCGATAGAT TGTGCACCT GATTGCCCGA CATTATCGCG AGCCCATTAA TACCCATATA 1500
AATCAGCATH CATGTTGGAA TTTAATCGCG GCCTAGAGCA AGACGTTCC CGTTGAATAT 1560
GGCTCATAAC ACCCCTTGTA TTACTGTTA TGTAAGCAGA CAGTTTATT GTTCATGACC 1620
AAAATCCCTT AACGTGAGTT TTCGTTCCAC TGAGCGTCAG ACCCCGTAGA AAAGATCAA 1680
GGATCTTCTT GAGATCCTTT TTTCTGCGC GTAATCTGCT GCTTGCAAAC AAAAAAACCA 1740
CCGCTACCAAG CGGTGGTTG TTTGCCGGAT CAAGAGCTAC CAACTCTTT TCCGAAGGTA 1800
ACTGGCTTCA GCAGAGCGCA GATAACAAAT ACTGTCCTTC TAGTGTAGCC GTAGTTAGGC 1860
CACCACTTCA AGAAACTCTGT AGCACCGCCT ACATACCTCG CTCTGCTAAT CCTGTTACCA 1920
GTGGCTGCTG CCAGTGGCGA TAAAGTCGTGT CTTACCGGGT TGGACTCAAG ACGATAGTTA 1980
CCGGATAAGG CGCAGCGGTC GGGCTGAACG GGGGGTTCGT GCACACAGCC CAGCTTGGAG 2040
CGAACGACCT ACACCGAACT GAGATACCTA CAGCGTGAGC TATGAGAAAG CGCCACGCTT 2100
CCCGAAGGGA GAAAGGCGGA CAGGTATCCG GTAAGCGGCA GGGTCGGAAC AGGAGAGCGC 2160
ACGAGGGAGC TTCCAGGGGG AAACGCCTGG TATCTTATA GTCCTGTCGG GTTTCGCCAC 2220
CTCTGACTTG AGCGTCGATT TTTGTGATGC TCGTCAGGGG GGCGGAGCCT ATGGAAAAAC 2280
GCCAGCAACG CGGCCTTTT ACGGTTCCTG GCCTTTGCT GGCCTTTGC TCACATGTT 2340
TTTCCTGCGT TATCCCCTGA TTCTGTGGAT AACCGTATTA CCGCCTTGTA GTGAGCTGAT 2400
ACCGCTCGCC GCAGCCGAAC GACCGAGCGC AGCGAGTCAG TGAGCGAGGA AGCGGAAGAG 2460
CGCCTGATGC GGTATTTCT CCTTACGCAT CTGTGCGGTAA TTTCACACCG CATATATGGT 2520
GCACTCTCAG TACAATCTGC TCTGATGCCG CATAAGTTAAG CCAGTATACA CTCCGCTATC 2580
GCTACGTGAC TGGGTCATGG CTGCGCCCCG ACACCCGCCA ACACCCGCTG ACGCGCCCTG 2640
ACGGGCTTGT CTGCTCCGG CATCCGCTTA CAGACAAGCT GTGACCGTCT CCGGGAGCTG 2700
CATGTGTCAG AGGTTTCAC CGTCATCACC GAAACGCGCG AGGCAGCTGC GGTAAAGCTC 2760

Figure 8C (Continued)

(SEQ ID NO:62)

ATCAGCGTGG TCGTGAAGCG ATTACACAGAT GTCTGCCTGT TCATCCGCGT CCAGCTCGTT 2820
GAGTTTCTCC AGAACGCGTTA ATGTCTGGCT TCTGATAAAAG CGGGCCATGT TAAGGGCGGT 2880
TTTTTCCTGT TTGGTCACTG ATGCCTCCGT GTAAGGGGGA TTTCTGTTCA TGGGGGTAAT 2940
GATACCGATG AAACGAGAGA GGATGCTCAC GATACGGGTT ACTGATGATG AACATGCCCG 3000
GTTACTGGAA CGTTGTGAGG GTAAACAACG GGCGGTATGG ATGCGGCCGG ACCAGAGAAA 3060
AATCACTCAG GGTCAATGCC AGCGCTTCGT TAATACAGAT GTAGGTGTTG CACAGGGTAG 3120
CCAGCAGCAT CCTGCGATGC AGATCCGGAA CATAATGGTG CAGGGCGCTG ACTTCCGCGT 3180
TTCCAGACTT TACGAAACAC GGAAACCGAA GACCATTCA CATTTGCTC AGGTGGCAGA 3240
CGTTTGCGAG CAGCAGTCGC TTCACGTTCG CTCGCGTATC GGTGATTCA TCTGCTAAC 3300
AGTAAGGCAA CCCC GCCAGCAGC CTAGCCGGT CCTCAACGAC AGGAGCACGA TCATGCGCAC 3360
CCGTGGGCCGCC GCCATGCCGG CGATAATGGC CTGCTTCTCG CCGAAACGTT TGGTGGCGGG 3420
ACCAGTGACG AAGGCTTGAG CGAGGGCGTG CAAGATTCCG AATACCGCAA GCGACAGGCC 3480
GATCATCGTC GCGCTCCAGC GAAAGCGGTC CTCGCCGAAA ATGACCCAGA GCGCTGCCGG 3540
CACCTGTCCT ACGAGTTGCA TGATAAAAGAA GACAGTCATA AGTGCAGCGA CGATAGTCAT 3600
CCCCCGCGCC CACCGGAAGG AGCTGACTGG GTTGAAGGCT CTCAAGGGCA TCGGTGAGA 3660
TCCCGGTGCC TAATGAGTGA GCTAACTTAC ATTAATTGCG TTGCGCTCAC TGCCCGCTTT 3720
CCAGTCGGGA AACCTGTCGT GCCAGCTGCA TTAATGAATC GGCCAACGCG CGGGGAGAGG 3780
CGGTTTGCCT ATTGGCGGCC AGGGTGGTT TTCTTTCAC CAGTGAGACG GGCAACAGCT 3840
GATTGCCCTT CACCGCCTGG CCCTGAGAGA GTTGCAGCAA GCGGTCCACG CTGGTTGCC 3900
CCAGCAGGCC AAAATCCTGT TTGATGGTGG TTAACGGCGG GATATAACAT GAGCTGTCTT 3960
CGGTATCGTC GTATCCCAC ACCGAGATAT CCGCACCAAC GCGCAGCCCG GACTCGGTAA 4020
TGGCGCGCAT TGCGCCCAGC GCCATCTGAT CGTTGGCAAC CAGCATCGCA GTGGGAACGA 4080
TGCCCTCATT CAGCATTGCA ATGGTTGTT GAAAACCGGA CATGGCACTC CAGTCGCCTT 4140

Figure 8C (Continued)

(SEQ ID NO:62)

DRAFT - 20150602

CCCGTTCCGC TATCGGCTGA ATTTGATTGC GAGTGAGATA TTTATGCCAG CCAGCCAGAC 4200
GCAGACGCGC CGAGACAGAA CTTAATGGGC CCGCTAACAG CGCGATTGC TGGTGACCCA 4260
ATGCGACCAG ATGCTCCACG CCCAGTCGCG TACCGTCTTC ATGGGAGAAA ATAATACTGT 4320
TGATGGGTGT CTGGTCAGAG ACATCAAGAA ATAACGCCGG AACATTAGTG CAGGCAGCTT 4380
CCACAGCAAT GGCATCCTGG TCATCCAGCG GATAGTTAAT GATCAGCCCA CTGACGCGTT 4440
GCGCGAGAAG ATTGTGCACC GCCGCTTAC AGGCTTCGAC GCCGCTTCGT TCTACCATCG 4500
ACACCACCAC GCTGGCACCC AGTTGATCGG CGCGAGATTT AATCGCCGCG ACAATTGCG 4560
ACGGCGCGTG CAGGGCCAGA CTGGAGGTGG CAACGCCAAT CAGCAACGAC TGTTTGCCCC 4620
CCAGTTGTTG TGCCACGCGG TTGGGAATGT AATTCAAGCTC CGCCATCGCC GCTTCCACTT 4680
TTTCCCGCGT TTTCGCAGAA ACGTGGCTGG CCTGGTTCAC CACGCGGGAA ACGGTCTGAT 4740
AAGAGACACC GGCATACTCT GCGACATCGT ATAACGTTAC TGGTTTCACA TTCACCACCC 4800
TGAATTGACT CTCTTCCGGG CGCTATCATG CCATACCGCG AAAGGTTTG CGCCATTCGA 4860
TGGTGTCCGG GATCTCGACG CTCTCCCTTA TGCGACTCCT GCATTAGGAA GCAGCCCAGT 4920
AGTAGGTTGA GGCGGTTGAG CACCGCCGCC GCAAGGAATG GTGCATGCAA GGAGATGGCG 4980
CCCAACAGTC CCCCGGCCAC GGGGCCTGCC ACCATACCCA CGCCGAAACA AGCGCTCATG 5040
AGCCCGAAGT GGCGAGCCCG ATCTTCCCCA TCGGTGATGT CGCGATATA GGCGCCAGCA 5100
ACCGCACCTG TGGCGCCGGT GATGCCGGCC ACGATGCGTC CGGCGTAGAG GATCGAGATC 5160
GATCTCGATC CCGCGAAATT AATACGACTC ACTATAAGGGG AATTGTGAGC GGATAACAAT 5220
TCCCCTCTAG AAGTCGACTT TAAGAAGGAG TACCAAG ATG CCT GAG GAA AGT CAG 5275
GAG ACA TTC GAA GAT CTA TGG AAA CTA CTT CCT GGT CAC CAC CAC CAT 5323
CAC CAT GGT ATG AGC GGC GGC ATG GAG GAG CCC AGT GAC CTT GAG GAG 5371
CTC GAG CAG TTT GCC AAG ACC TTC AAA CAA AGA CGA ATC AAA CTT GGA 5419
TTC ACT CAG GGT GAT GTT GGG CTC GCT ATG GGG AAA CTA TAT GGA AAT 5467

Figure 8C (Continued)

(SEQ ID NO:62)

GAC TTC AGC CAA ACT ACC ATC TCT CGA TTT GAA GCC TTG AAC CTC AGC	5515
TTT AAG AAC ATG TGC AAG TTG AAG CCA CTT TTA GAG AAG TGG CTA AAT	5563
GAT GCA GAG AAC CTC TCA TCT GAT TCG TCC CTC TCC AGC CCA AGT GCC	5611
CTG AAT TCT CCA GGA ATT GAG GGC TTG AGC AGG CGC CGT AAG AAA CGC	5659
ACC AGC ATA GAG ACC AAC ATC CGT GTG GCC TTA GAG AAG AGT TTC TTG	5707
GAG AAT CAA AAG CCT ACC TCG GAA GAG ATC ACT ATG ATT GCT GAT CAG	5755
CTC AAT ATG GAA AAA GAG GTG ATT CGT GTT TGG TTC TGT AAC CGT CGA	5803
CAG AAA GAA AAA AGA ATC AAC CCA CAG CCA GAA CTC GCC CCG GAA GAC	5851
CCC GAG GAT TAGGATCCGA ATT	5873

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Phosphorylation of Recombinant Substrates by Purified Human DNA-PK

FIGURE 9

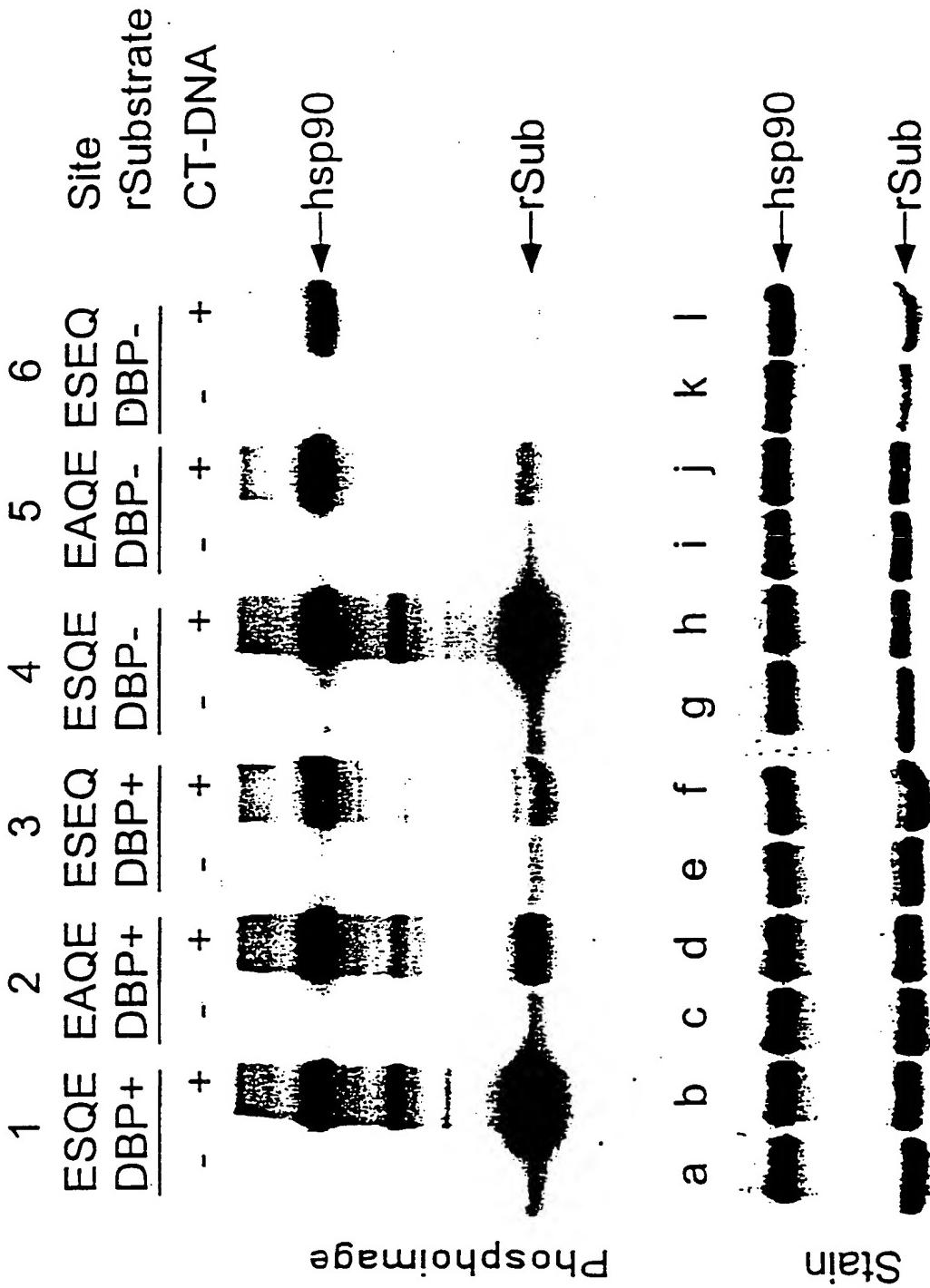


FIGURE 10

Isoelectrofocusing Analysis of Recombinant DNA-PK Substrates

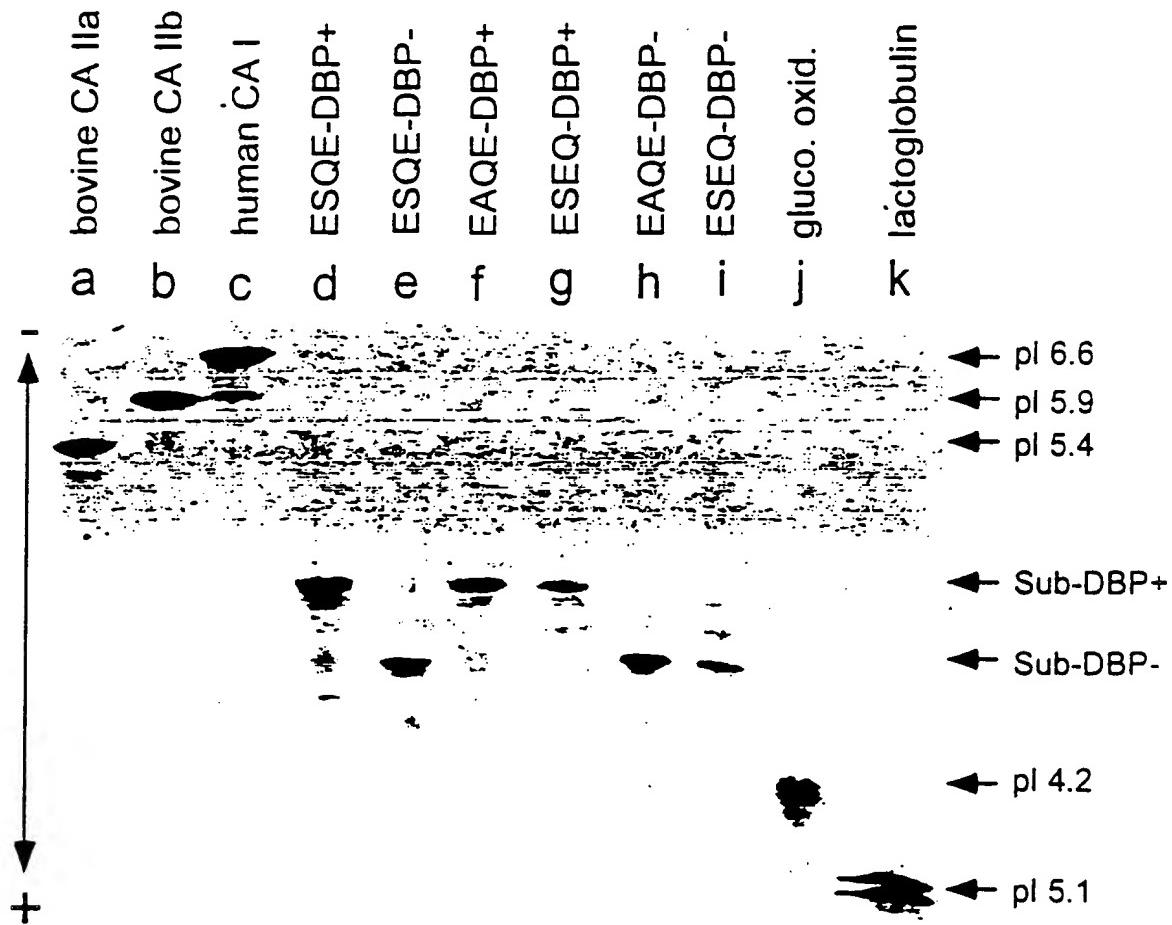


FIGURE 11

